

SEQUENCE LISTING

<110> MINAMINO, NAOTO
KATAFUCHI, TAKESHI

<120> NOVEL PEPTIDES HAVING cAMP PRODUCING ACTIVITY

<130> 62273 (71526)

<140> 10/516,768

<141> 2004-12-03

<150> PCT/JP03/06641

<151> 2003-05-28

<150> JP 2002-162797

<151> 2002-06-04

<160> 52

<170> PatentIn Ver. 3.3

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 <213> Sus sp.

<220>
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 Gly Ser Lys Val Leu
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 Met Gly
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 ttc tgg aag ttc ccc ccc ttc ctg atc ctc agc atc ctg gtc ctg tac 165
 Phe Trp Lys Phe Pro Pro Phe Leu Ile Leu Ser Ile Leu Val Leu Tyr
 5 10 15
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 Gln Ala Gly Met Leu His Ala Ala Pro Phe Arg Met Ala Leu Gly Ser
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agc ttt gat tct gcc aca ctc acg gaa gag gaa atg tcc ctc cta ctg      261
Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Glu Met Ser Leu Leu Leu
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gtt gca atg gtg aag gat tat gtg cag atg aag gcc act gtg ctg gag      309
Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val Leu Glu
                    55                      60                      65

cag gag aca gag gac ttc agc atc acc acc cag gag aga tcc tgc aac      357
Gln Glu Thr Glu Asp Phe Ser Ile Thr Thr Gln Glu Arg Ser Cys Asn
                    70                      75                      80

act gcc atc tgt gtg acc cac aag atg gca ggc tgg ctg agc aga tct      405
Thr Ala Ile Cys Val Thr His Lys Met Ala Gly Trp Leu Ser Arg Ser
                    85                      90                      95

ggg agc gtg gtt aag aac aac ttc atg ccc atc aac atg ggc tcc aaa      453
Gly Ser Val Val Lys Asn Asn Phe Met Pro Ile Asn Met Gly Ser Lys
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gtc ttg ggc cgg cgc cgc aga cag cct cag gcc tgagctgtga aatgactcta      506
Val Leu Gly Arg Arg Arg Arg Gln Pro Gln Ala
115                      120                      125

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accaatttga aaaatagcat ggaagacaca catatatgca tgcttcttgc ttgaaataca      626

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Leu Tyr Gln Ala Gly Met Leu His Ala Ala Pro Phe Arg Met Ala Leu
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Gly Ser Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Glu Met Ser Leu
    35                      40                      45

Leu Leu Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val
    50                      55                      60

Leu Glu Gln Glu Thr Glu Asp Phe Ser Ile Thr Thr Gln Glu Arg Ser
    65                      70                      75                      80

Cys Asn Thr Ala Ile Cys Val Thr His Lys Met Ala Gly Trp Leu Ser
                85                      90                      95

Arg Ser Gly Ser Val Val Lys Asn Asn Phe Met Pro Ile Asn Met Gly
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Ser Lys Val Leu Gly Arg Arg Arg Arg Gln Pro Gln Ala
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 Val Asn Lys Phe Tyr Ala Phe Pro Leu Thr Thr Thr Gly Ile Arg Val
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Ser

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 Met Gly
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 Phe Trp Lys Phe Pro Pro Phe Leu Ile Leu Ser Ile Leu Val Leu Tyr
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 caa gca gga atg ctc cat gcc gcg cca ttc agg atg gct ttg gga agc 213
 Gln Ala Gly Met Leu His Ala Ala Pro Phe Arg Met Ala Leu Gly Ser
 20 25 30
 agc ttt gat tct gcc aca ctc acg gaa gag gaa atg tcc ctc cta ctg 261
 Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Met Ser Leu Leu Leu
 35 40 45 50

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gtt gca atg gtg aag gat tat gtg cag atg aag gcc act gtg ctg gag      309
Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val Leu Glu
                    55                                60                                65

cag gag aca gag gac ttc agc ctg gac agc tcc aga gct aag cag tgc      357
Gln Glu Thr Glu Asp Phe Ser Leu Asp Ser Ser Arg Ala Lys Gln Cys
                    70                                75                                80

aat aat ctg agt acc tgt gtg ctg gga aca tat aca tgg gac gtc aac      405
Asn Asn Leu Ser Thr Cys Val Leu Gly Thr Tyr Thr Trp Asp Val Asn
                    85                                90                                95

aag ttt tat gca ttc ccc tta act aca act ggg att aga gta tct ggc      453
Lys Phe Tyr Ala Phe Pro Leu Thr Thr Thr Gly Ile Arg Val Ser Gly
                    100                                105                                110

aag aaa tgg gtc agg gcc aga gtc tca gag aaa gtc cat tat ccc tca      501
Lys Lys Trp Val Arg Ala Arg Val Ser Glu Lys Val His Tyr Pro Ser
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agg cag cat acc cta agg tgc tta aga agg ccc cca ccc ctc ctc ctt      549
Arg Gln His Thr Leu Arg Cys Leu Arg Arg Pro Pro Pro Leu Leu Leu
                    135                                140                                145

tct agt tcc tct cct aga att tgc atg tgt tct tct ctg gtt gct ctc      597
Ser Ser Ser Ser Pro Arg Ile Cys Met Cys Ser Ser Leu Val Ala Leu
                    150                                155                                160

tgagctgcta tcagcagctt tccttgtggc catggatgtc tggaatatca gagaggaggt      657

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<210> 21
 <211> 162
 <212> PRT
 <213> Sus sp.

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<400> 21
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          20          25          30

Gly Ser Ser Phe Asp Ser Ala Thr Leu Thr Glu Glu Glu Met Ser Leu
          35          40          45

Leu Leu Val Ala Met Val Lys Asp Tyr Val Gln Met Lys Ala Thr Val
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Leu Glu Gln Glu Thr Glu Asp Phe Ser Leu Asp Ser Ser Arg Ala Lys
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<211> 7142
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<213> Sus sp.
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 Gly Ser Glu Ala Phe
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Ser Arg Ser Gly Gly Val Val Lys Asn Asn Phe Val Pro Thr Asn Val
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Gly Ser Lys Ala Phe
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